CLAIMS

1. A method for designing a compound capable of binding to an active site, an accessory binding site or a pocket of an RRF protein, which comprises computationally evaluating a chemical entity of RRF protein on the basis of a structure coordinate obtained from an RRF protein crystal.

2. The method according to claim 1, wherein the RRF protein crystal is any crystal of the RRF protein itself, an RRF protein mutant, an RRF protein homologue or an RRF protein co-complex.

3. The method according to claim 1 or 2, wherein the RRF protein crystal is bipyramidal.

4. The method according to any one of claims 1 to 3, wherein the RRF protein crystal has a space group $P4_12_12_1$ or a space group $P4_32_12$.

5. The method according to any one of claims 1 to 4, wherein the RRF protein crystal has a size of 0.3 × 0.3 × 0.5 mm.

6. The method according to any one of claims 1 to 5, wherein the RRF protein crystal has respective unit lattices of a size of a=b=47.3Å and c=297.6Å.

7. The method according to any one of claims 1 to 6, wherein the RRF protein crystal is characterized by a structure coordinate described in Table 7.

8. The method according to claims 1 to 7, wherein the RRF protein crystal is derived from Thermotoga Maritima.

9. The method according to any one of claim 1 or 2, wherein the RRF protein crystal is orthorhombic.

10. The method according to any one of claims 1, 2 and 9, wherein the RRF protein crystal has a space group $P2_12_12$.

11. The method according to any one of claims 1 to 2 and 9 to 10, wherein the RRF protein crystal has a size of 30 x 50 x 250 μm.

12. The method according to any one of claims 1 to 2 and 9 to 11, wherein the RRF protein crystal is derived from strain X.

13. The method according to any one of claims 1 to 12, wherein the RRF protein crystal is crystallized by a drop-like vapour diffusion method.

14. The method according to any one of claims 1 to 13, wherein the RRF protein crystal is a heavy atom derivative and the crystal is any crystal of the RRF protein itself, an RRF protein mutant, an RRF protein homologue or an RRF protein co-complex.

15. The method according to any one of claims 1 to 14, wherein the heavy atom derivative is formed by reaction of a compound selected from the group consisting of thyromethal, gold thiomalate, uranyl acetate and lead chloride.

16. The method according to any one of claims 1, 2 and 9 to 12, wherein the RRF protein crystal is a heavy atom derivative of platinum or mercury.

17. The method according to any one of claims 1 to 16, wherein the RRF protein is a monomer.

18. The method according to any one of claims 1 to 8, 13 to 15 and 17, wherein the RRF protein is characterized by amino acid displacement according to Table 5 or Table 6.

19. The method according to any one of claims 1 to 18, wherein a compound characterized by the chemical entity bound to the active site, accessory binding site or pocket is an inhibitor to the RRF

protein.

20. The method according to any one of claims 1 to 19, wherein the inhibitor is a competitive inhibitor, an uncompetitive inhibitor or a noncompetitive inhibitor to the RRF.

21. The method according to any one of claims 1 to 20, comprising determining orientation of a ligand at the active site or accessory binding site of the RRF protein.

22. The method according to any one of claims 1 to 8, 13 to 15 and 17 to 21, wherein the structure coordinate is a structure coordinate of the RRF protein according to Table 7.

23. A method for determining a three-dimensional structure of an RRF protein, comprising elucidating crystal form of a mutant, homologue or co-complex of the RRF protein by molecular replacement.

24. An RRF protein crystal which is orthorhombic.

25. The RRF protein crystal according to claim 24, having a space group $P2_12_12$.

26. The RRF protein crystal according to claim 24 or 25, having

a size of 30 × 50 × 250 μm.

27. The RRF protein crystal according to any one of claims 24 to 26, wherein the RRF is derived from strain X.

28. The RRF protein crystal which is bipyramidal.

29. The RRF protein crystal according to claim 28, wherein the RRF protein crystal has a space group $P4_12_12_1$ or a space group $P4_32_12$.

30. The RRF protein crystal according to claim 28 or 29, having a size of 0.3 × 0.3 × 0.5 mm.

31. The RRF protein crystal according to any one of claims 28 to 30, having respective unit lattices of a size of a=b=47.3Å and c=297.6Å.

32. The RRF protein crystal according to any one of claims 28 to 31, characterized by amino acid displacement according to Table 5 or Table 6.

33. The RRF protein crystal according to any one of claims 28 to 32, characterized by a structure coordinate according to Table 7.

34. The RRF protein crystal according to any one of claims 28 to 33, derived from Thermotoga Maritima.

35. The RRF protein crystal according to any one of claims 24 to 34, crystallized by a drop-like vapour diffusion method.

36. The RRF protein crystal according to any one of claims 24 to 35, wherein the crystal is any crystal of the RRF protein itself, an RRF protein mutant, an RRF protein homologue or an RRF protein co-complex.

37. An RRF protein, wherein amino acid in an active site is selected from the group consisting of Arg 110, Arg 129 and Arg 132 of SEQ. ID. NO. 1.

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38. The RRF protein according to claim 37, wherein at least one amino acid in the active site or accessory active site is replaced by at least one amino acid selected from the group consisting of naturally occurring amino acids, non-natural amino acids, selenocysteine and selenomethionine.

39. The RRF protein according to claim 37, wherein a hydrophilic amino acid or a hydrophobic amino acid in the active site or accessory active site is replaced.

40. The RRF protein according to claim 37, wherein at least one cysteine amino acid is replaced by an amino acid selected from the group consisting of selenocysteine and selenomethionine.

41. The RRF protein according to claim 37, wherein at least one methionine amino acid is replaced by an amino acid selected from the group consisting of selenocysteine or selenomethionine.

42. The RRF protein according to any one of claims 37 to 38, wherein the RRF protein is in a crystal form.

43. The RRF protein according to claim 37, having a specific activity higher or lower than that of a wild type enzyme.

44. The RRF protein according to claim 37, having a varied substrate specificity.

45. Use of an RRF protein according to claim 37 for measuring binding interaction between a compound and the RRF protein.

46. The RRF protein according to claim 37, wherein at lest one amino acid residue on a surface of the RRF protein, in the surface or in the vicinity thereof is replaced and a change in surface charge

by one or more charge units occurs.

47. The method according to any one of claims 1 to 22, wherein the pocket of the RRF protein is a pocket in the vicinity of C-terminal positioned on a folded part separating two domains of the RRF protein.

48. The method according to any one of claims 1 to 22, wherein the compound inhibits binding of the RRF protein to ribosome or inhibits behavior of the RRF protein on the ribosome.

49. The inhibitor to an RRF protein, obtained by the method according to any one of claims 19 to 23, 47 and 48.

50. A method for searching a compound that can inhibit activity of an RRF protein on the basis of its activity of inhibiting binding of the RRF protein to ribosome or its activity of inhibiting behavior of the RRF protein on the ribosome.

51. An inhibitor to an RRF protein, obtained by the method according to claim 50.